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          SREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 234
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APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: A Protein Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADRESS:
ADDRESSE: Calfae, Halter & Griswold LLP
STREET: 1400 McDdaald Investment Center, 800 Superior
STREET: Avenue
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, WARPLICATION DATA:
APPLICATION NUMBER: US/09/062,440
ETLING DATE:
CLASSIFICATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6207422
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NAME: DOCHETLY, Pamela A.
REGISTRATION NUMBER: 40591
REFRENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION.
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STRANDEDNESS: not relevant
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STATE: Ohio
COUNTRY: US
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APPLICANT: Edughn, Mariah, R.
TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
CURRENT APPLICATION NUMBER: US/09/836,941
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/286,132
PRIOR PILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
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Pred. No. 7.5e-266;
7; Mismatches 14;
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Partent NG. 6465200
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US-09-836-941-2
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Best Local Similarity 96.3
Matches 553; Conservative
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APPLICANT: Kaser, Mariah, R.
TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY ITLLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY US
CURRENT APPLICATION NUMBER: US/09/286,132
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGRAM
SEQ ID NO 2
   14;
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Pred. No. 7.5e-266;
7; Mismatches 14;
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Best Local Similarity 96.3%;
Matches 553; Conservative 7
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    553; Conservative
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US-09-286-132-2
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                                                  574;
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7; Mismatches 14:
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APPLICANT: Wible, Barbara
APPLICANT: Wible, Barbara
APPLICANT: Wible, Barbara
TITLE OF INVENTION: Protein That Enhances Exprint OF INVENTION: and Nucleic Acids That Englisher APPLICATION NUMBER: US/09/712,495
CURRENT FILING DATE: 2000-11-14
PRIOR PILING DATE: 2988-04-17
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Patent No. 6391561
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                   1 MKIKELYRRRFPRKTLGPS
                                                Query Match 96.7%;
Best Local Similarity 96.3%;
Matches 553; Conservative
         protein
                                                                                                            1 MKIKELYRRFPR
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Best Local Similarity
      ; -MOLECULE TYPE:
US-09-062-440-4
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                  SEVCPPPGYGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDLPPTKKHCSVTSAA
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LOMNEKKPTWTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGSWCPMKPKKEA
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APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Oing
APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER PERCENDENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: AALTER & Griswold LLP
STREET: 4400 McDonald Investment Center, 800 Superior
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(400 McDonald Investment Center, 800 Superior
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SYSTEM: Pt-DOS/MS-DOS
Patentin Ralease #1.0, Version #1.30
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NAME: DOCHETY, Pamela A.
REGISTRATION NUMBER: 20591
REFERENCE/DOCKET NUMBER: 2288
TELECOMMUNICATION INFORMATION:
TELECPHONE: 216228200
TELEPHONE: 2162410816
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APPLICATION NUMBER: UI
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 574 amino acids TYPE: amino acid
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COMPUTER READABLE MEDIUM TYPE: Flor
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APPLICANT: Kaser, Matthew, R.
APPLICANT: Raughn, Mariah, R.
TITLE OF INFORMATION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
FILE REFERENCE: PC-0001 US
CURRENT APPLICATION NUMBER: US/09/836,941
CURRENT APPLICATION NUMBER: 09/286,132
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGram
SEQ ID NO 2
LENGTH: 628
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100.0%; Pred. No. 2.2e-272;
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Patent No. 6465200
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ORGANISM: Homo sapiens
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Matches 574;
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US-09-836-941-2
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                                                                                            181 PKRPSRPINITPLARLSATVPNTIVVNMSSEFGRNYSLSVYLVRQLTAGTLLQKLRAKGI
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APPLICANT: Yang, Ging
APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBAR OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALGRee, Halter & Griswold LLP
STREET: 4400 McDonald Investment Center, 800 Superior
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APPLICATION NUMBER: US/09/062,440
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
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CLASSTRICATION:
CLASSTRICATION:
ATTORNEY AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/POCKET NUMBER: 228
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Obio
COUNTRY: US
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US-09-062-440-6
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Sequence 2, Application US/09712495
Sequence 2, Application US/09712495
Sequence 2, Application US/09712495
Sequence 3, Application US/09712495
GENERAL INFORMATION:
SEQUENCE 3, APPLICANT: Wible, Barbara
APPLICANT: Yang, Oing
APPLICANT: Yang, Oing
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 22884/04046
CURRENT APPLICATION NUMBER: US/09/712,495
CURRENT PILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/062,440
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFWWARE: Patentin Version 3.0
SEQ ID NO 2.
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Pred. No. 3.9e-262;
7; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.3
Matches 553; Conservative
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APPLICANT: Baughn, Mariah, R.
TILLE OF INVENTED TO TRANSCRIPTION FACTOR REGULATORY PROTEIN
FILE REFERENCE: PC-0001 US
CURRENT APPLICATION NUMBER: US/09/836,941
CURRENT APPLICATION NUMBER: 09/286,132
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGRAM
SEQ ID NO 2
LENGTH: 628
                                                                                                                                                                                                                       Score 544; DB 3; Length 628;
Pred. No. 2.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 544; DB 4; Length 628; Best Local Similarity 100.0%; Pred. No. 2.3e-54; Matches 99; Conservative 0; Mismatches 0; Indels (
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Barbara A.
NN A Protein that Enhances Expression of
DN: Octassium Channels on Cell Surfaces
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CURRANT APPLICATION NUMBER: US/09/286,132
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGRAM
SEQ ID NO 2
LENGTH: 628
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100.08; 0; Pr
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Patent No. 620/422
GENERAL INFORMATION:
APPLICANT: BROWN, Arthur M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09836941 Patent No. 6465200, GENERAL INFORMATION:
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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; OTHER INFORMATION: 2667068
US-09-836-941-2
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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ORGANISM: Homo sapiens
                                                                                                                                                                 CTHER INFORMATION:
US-09-286-132-2
                                                                                                                                ORGANISM: Homo
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APPLICANT:
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                                                                                                                  TYPE: PRT
                                                                                                                                                 FEATURE:
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E: Calfee, Halter & Griswold LLP
1400 McDonald Investment Center, 800 Superior
Avenue
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                                                                                                                                                                                 OPERATUNG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,440
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LOCATION: 416..417
OTHER INFORMATION: /note= "serine or proline"
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                                                                                                                                                                                                                                                                                                                                                                22884/04004
                                                                                                                                                                                                                                                               FILING DATA:
CLASSIFICATION:
ATTORNEY/AGENT\, INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKEY NUMBER: 228
                                                                                                                                                  : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION NIFORMATION TELEPHONE: 2166228200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 574 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 37..38
OTHER INFORMATION: /no
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 216228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTIES:
                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
LOCATION: 383..384
OTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 335..336
OTHER INFORMATION:
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NAME/KEY: Peptide
LOCATION: 381..382
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 41..42
OTHER INFORMATION:
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                                                 CITY: Cleveland
STATE: Ohio
                                                                                                              44114
   ADDRESSEE:
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                                                                                            COUNTRY:
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Sequence 7, Application US/09712495
Patent NO 6391561
GENERAL INPORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Brown, Arthur
APPLICANT: Withe, Barbara
APPLICANT: Wither Expension of Potassium Channels on Cell S
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 2084/04046
CURRENT APPLICATION NUMBER: US/05/12,495
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Version 3.0
ENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/062,440
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Pred. No. 2.8e-52;
3; Mismatches 2.
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Pred. No. 2.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DOCHERTY, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 2281
TELEPHONE: 216528200
TELEPHONE: 216528200
TELEPHONE: 21652800
TELEPHON
                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss: not relevant
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Best Local Similarity 94.9%;
Matches 94; Conservative
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Best Local Similarity 94.9%;
Matches 94; Conservative
                                                                                                                   ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                             Cleveland
Ohio
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-09-062-440-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-742-495-7
                                                                                               COUNTRY:
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Patent No. 6207422
GENERAL INFORMATION:
APPLICANT: Brown Arthur M.
APPLICANT: Yang, Oing
APPLICANT: Yang, Oing
APPLICANT: Parior Oing
APPLICANT: Parior Oing
APPLICANT: Parior Oing
APPLICANT: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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STREET: 1400 McDonald Investment Center, 800 Superior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 YGLDGLQYSPVQXGXPSENKKXXXEVIDLTIESSSDEEDL 407
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LOCATION: 570..571

CTHER INFORMATION: /note= "isoleucine or valine"

US-09-062-440-6
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 501..502
OTHER INFORMATION: /note= "alaqine or threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "cysteine or arginine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: Peptide
LOCATION: 535..536
OTHER INFORMATION: /note= "proline or alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Peptide
LOCATION: 547..548
OTHER INFORMATION: /note= "glycine or serine"
FRATURE:
FEATURE:
NAME/KEY: Peptide
LOCATION: 431..432
CTHER INFORMATION: /note= "valine or alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
LOCATION: 513..514
OTHER INFORMATION: /note= "serine or proline"
NAME/KEY: Peptide
LOCATION: 5.28..529
OTHER INFORMATION: /note= "cysteine or argini
                                                                                                                                                           NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
                                                                                                                                                                                                                                                                                                                                                    /note= "glycine or serine'
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Pred. No. 1.2e-51;
0; Mismatches 4
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NAME/KEY: Peptide
LOCATION: 508.509
OTHER INFORMATION: /note= "tyrosine of
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Best Local Similarity 96.0%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                         LOCATION: 489.490
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY:
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US-09-062-440-7
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SREVLPGAKCDYIIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 190
                                                                                                                                                                                                                             AHLQSFSAALYLQMNE-KPTWTCPVCDKKAPWESLIIDGLFMEILXSCSDCDEIQFMEDG 348
                                                                                                                                                                                                                                                                                                                                                                                                                             419 TKKHCPVTSAAIPALPGSKGALTSGHQPSSVLRSPAMGTLGSDFLSSLPVHEYPPAFPLG 478
                                                                                                     ---SLLIGHLSLDG--ITPCPCLVRQLTAG
                                                                                                                                                                                                                                                AHLQSFDAALYLQMNEKKPTWTCPVCDKKAPYESLIIDGLFMEILNSCSDCDEIOFMEDG
                                                                                                                                                                                                                                                                                                           STCPMKPKKEASEVCPPPGYGLDGLQYSPVQXGXPSENKKXVEVIDLTIESSSDEEDLPP
                                                                                                                                                                                                                                                                                                                                      359 SWCPMKPKKEASEVCPPFGYGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPP
                                                             --SRPINITPKARLSATVPNTIVVNWSSEFGRNTSLSVYLVRQLTAG
                                                                                                                                             TLLQKLRAKGIRNPDHSRALIKGKLTADPDSGVATTSLRVSLMCPLGKMRLTVPCRALTC
                                                                                                                                                                          TLLQKLRAKGIRNPDHSRALIKEKLTADPDSEVATTSLPGVTHVPARKMRLTVPCRALTC
                                                                                                                                                                                                                                                                                                                                                                                           TKKHCXVTSAAIPALPGSKGXLTSGHQPSSVLRSPAMGTLGXDFLSSLPLHEYPPAFPLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/399,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.3%; Score 1480.5; DB 1; 53.1%; Pred. No. 2.3e-138; iive 77; Mismatches 152;
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FILING DATE:

CLASSIFICATION: 435
CLASSIFICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

APTORNEY/AGENT INFORMATION.

RAGISTRATION NUMBER: 30,223.

REFERENCE/DOCKET NUMBER: 1552-0007
TELECHONE: (415) 326-242

TELEPHONE: (415) 326-242

INFORMATION FOR SEQ ID NO: 102:

GEOTIFNICE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMBER: US/08/399,696
02c,MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 102, Application US/08399696; Patent No. 575669; GENERAL INFORMATION:
                                                                                                     PRGPAVRSTSHPWLDSQPLSPTP
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Best Local Similarity 53.1°
Matches 326, Conservative
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TITLE OF INVENTION: POLY
NUMBER OF SEQUENCES: 128
COMPUTER READABLE FORM:
MEDLUM, TYPE: Floppy di
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TOPOLOGY: unk
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                           --PVHPDVIMKPLPFYEVYGELIRPTILASTSSQRFEEAHFTFALTPQQLQQILT 130
                                                                                                                                                                                                                                                                              TLLQKLRAKGIRNPDHSRALIKEKLTADQDSEVATTSLPGVTHVPARKMRLTVPCRALTC 298
                                                                                                                                                                                                                                                                                                                                                 AHLQSFDAALYLQMNEKKPTWTCPVCDKKAPYESLINGGEFWEILNSCSDCDEIQFWEDG 358
                                                                                                                                                                                                                                                                                                                                                                                                                               TKKHCPVTSAAIPALPGSKGALTSGHQPSSVLRSPAMGTLGSDFLSSLPVHEYPPAFPLG 478
MHPPLPQPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQXQQILT 120
                                                                                QCAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 180
                                                                                                                      SREVLPGARCQYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 190
                                                                                                                                                                                                    ---SLLIGHLSLDG--ITPCPCLVRQLTAG 238
                                                                                                                                                                                                                                                                                                                                                                                                            STCPMKPKKEASEVCPPPGYGLDGLQYSPVQXGXPSENKKXVEVIDLTIESSSDEEDLPP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKHCXVTSAAIPALPGSKGXLTSGHQPSSVLRSPAMGTLGXDFLSŠLPLHEYPPAFPLG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQLQQILT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SREVLPGAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAB 180
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                                                                                                                                                                                                                                                                                                                            AHLQSFSAALYLQMNE-KPTWTCPVCDKKAPWESLIDGLFMEILXSCSDCDEIQFMEDG
                                                                                                                                                            SRPINITPKARLSATVPNTIVVNWSSEFGRNTSLSVYLVRQLTAG
                                                                                                                                                                                                                                            JTADPDSGVATTSLRVSLMCPLGKMRLTVPCRALTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADIQGLDLFSFLQTES-QYXPSVITSLDEQDXLGHFFQXRFTPXHFLGPLAPTLGSSHXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADIQGLDLFSFLQTESQQYGPSVIISLDEQDTLGHFFQYRGTPSHFLGPLAPTLGSCHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MHPPLPQPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQXQQILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKIKELYRRRFPRKTLGPSDLSLLSLPPGTSPVGSPXPLAXIPPTLLXPGTLLGPKREVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATPAPXPGRVSSIVAPGXXLREGHGGPLPSGPSLTGCRSDIXSLD 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPAPPPGRVSSIVAPGSSLREGHGGPLPSGPSLTGCRSDVISLD 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Easer, Matthew, R. APPLICANT: Easer, Mariah, R. TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN FILE REFERENCE: PC-0001 US CURRENT APPLICATION NUMBER: US/09/836,941 CURRENT FILING DATE: 2001-04-17 PRIOR PLLICATION NUMBER: 09/286,132 PRIOR PLLING DATE: 1999-04-01 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKIKELYRRRFPRKTLGPSDLSLLSLPPGTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09836941; Patent Mo. 6465200; GENERAL INFORMATION:
                                                                                                                                                                                                    191 PRGPAVRSTSHPWLDSQPDGPTP
                                                                                                                                                                                                                                            TLLQKLRAKGIRNPDHSRALIKÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: -
OTHER INFORMATION: 92689028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                            181 PKRP-----
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Best Local Similarity
Matches 462; Conserv
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LENGTH: 583
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GENERAL INFORMATION:
APPLICANT: Karpen, Gary H.
APPLICANT: Karpen, Gary H.
TITLE OF INVENTION: GENE INVOLVED IN CHROMOSOME INHERITANCE AND METHODS OF
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
CURRENT APPLICATION NUMBER: US/09/534,743
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,954
EARLIER APPLICATION NUMBER: 60/126,954
SARIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTING DATE: 2.1
SEQ ID NO 2
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                       60 ALTPÓQVQQISSSMDI-SGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNTKPCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAHLQSFSAALYLQMNB-KPTWTCPVCDKKAPWESLIIDGLFMEILXSCSDCDEIQFMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *XHFLGPLAPTLGSSHXSATPAPXPGRVSSIVAPGXXLREGHGGPLPS----GPSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 TSSQMFDAQLSAG-GSTSLPTTNGSSSGSNSSLVS-SNSLRESHSHTVTNRSSTDTASIF
                                                                                                                                                                                                                                            TIMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTF
                                                                                                                                                                                                                                                                1 LLGPKHELEL-PHLT8ÅLHPVHPDIKLQKLPFYDLLDELIKPTSLASDNSQRFRETCFAF
                                                                                                                                                                                                                                                                                                              ALTPOQXQQILTSREVLPGAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGKLCPL
                                                                                                                                                                                                                                                                                                                                                                                                               119 PGYLPPTKNGVEPKRPSRPINITSLVRLSTTVPNTIVVSWTAEIGRNYSMAVYLVKQLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GTLLQKLRAKGIRNPDHSRALIKGKLTADPDSGVATTSLRVSLMCPLGKMRLTVPCRALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTCPMKPKKEASEVCPPPGY-GLDG-----LQYSPVQXGXPSENKKXVEVIDLTIESSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 GTWAPMRSKKEVQEV--SASYNGVDGCLSSTLEHQVASHHQSSNKNKKVEVIDLTIDSSS
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                                                                                                                                                                                                       40;
                                                                                                                                                                  Length 539;
                                                                                                                                                                                                       Indels
                                                                                                                                                                47.1%; Score 1387; DB.T; 54.9%; Pred. No. 3,86-129; ive 69; Mismatches 139;
                                                                                                                                                                                                                                            52 LLGPKREVDMHPPLP---OPWHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-534-743-2; Sequence 2, Application US/09534743; Patent No. 6518400
122:
                                      539 amino acids
                                                                                                                                                                                                       Conservative
 INFORMATION FOR SEQ ID NO:
                                                                       unknown
                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572
                                                                                                        , MOLECULE TYPE: peptide US-08-399-696-122
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                                                                                             unknown
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                                                      amino acid
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Matches 302; Conserva
                                                                       STRANDEDNESS:
                                                                                           TOPOLOGY:
                                      LENGTH:
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                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| |::|||| || ::| | |::| | || || || IIDQDYRHPFHMTPMPYDLQGLDFFPFLSGDNQHYNTSLLAAAAAAVSDDQDLL---HSSR 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTP----XHFLGPLAPTLGSSHXSATPAPXPGRVSSIVAPGXXLREGHGGPLpg----G 558
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                                                                                                                                                                                                                         165 LCPLPGYLPPTKNOMEPKRPSRPINITPKARLSATVPNTIVVNWSSEFGRNTSLSVYLVR 224
                                                                                                                                                                                                                                                                                                    KGKLTADPDSGVATTSLRVSLMCPLGKMRLTVPC 284
                                                                                                                                                                                                                                                                                                                                                                                                             CLEMBILKYCTDCDBIQ 352
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                                                                                                                                                                                                                                                105 HPREALTPQQXQQILTSREVLPGAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGK
                                                                           48 XPGTLLGPKREVDMHPPLP---QPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSSDEEDLPPT-KKHCXVTSAAIPALPGSKGXLTSGHQPSSVLRSPAMGTLGXDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMEDGSTCPMKPKKEASEVCPPPGY-GLDG-----LQYSPVQXGXP
   MKIKELYRRRPPRKTLGPSDLSLLSLPPGTSPVGSPXPLAXIPPTL
                                                                                                                                                                                                                                                                                                                                                                                                     RALTCSHLOCFDATLYIOMNEKKPTWVCPVCDKKAPYEHLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53-BINDING POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                          RALTCAHLOSFSAALYLOMNE-KPTWTCPVCDKKAP
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy alsk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURENT APPLICATION DATA:
APPLICATION POWBER: US/08/399,696
FILING DATE: 02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,671
FILING DATE: 22-NOV-1993
ATTORNEY/ASPT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 122, Application US/08399696
Patent No. 5796669
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                    QLTAGTLLOKLRAKGIRNPDHSRAL
                                                                                                                                                                                                                                                            173 PCSLPGYLPPTKNGVEPKRPCR
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REGISTRATION NUMBER: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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OTHER INFORMATION: /note= "glycine or serine" PEATURE: \ NAME/KEY: Peptide

/note= "proline or

LOCATION: 41..42 OTHER INFORMATION: FEATURE:

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318 TWTCPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG 377
                                                                                                                                                                                                                                                                                                                                                                                              1 TWICPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG 60
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OOGICANIA SEL,
                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 516; DB 4; Length 583; Best Local Similarity 96.0%; Pred. No. 1.1e-52; Matches 95; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 YGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGLDGLQYSPVQEGNQSENKKRVEVIDLTIESSSDEEDL 99
                                                                                                                           CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION UNBER: 09/286,132
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGRAM
SEQ ID NO 17
LENGTH: 583
                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 92689028
US-09-836-941-17
                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            g
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/note= "tyrosine or phenylalanine" /note= "glycine or glutamic acid' /note= "isoproline or glutamine" /note= "alanine or threonine' /note= "serine or asparagine /note= "alanine or threonine /note= "cysteine or arginine /note= "proline or alanine" /note= "lysine or arganine /note= "valine or leucine' /note= "serine or proline' /note= "valine or alanine /note= "glycine or serine' /note= "glycine or serine' /note= "serine or proline' /note= "aspartic acid or asparagine" FEATURE:
NAME/KEY: Peptide
LOCATION: 381..382,
OTHER INFORMATION: FEATURE:
NAME/KEX: Peptide
LOCATION: 383..384
OTHER INFORMATION: 7
OTHER INFORMATION: 8 NAME/KEY: Peptide LOCATION: 384..385 OTHER INFORMATION: // NAME/KEY: Peptide LOCATION: 416..417 OTHER INFORMATION: / FEATURE: NAME/KEY: Peptide LOCATION: 501..502 OTHER INFORMATION: , FEATURE: NAME/KEY: Peptide LOCATION: 115..116 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 335,336 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 390.391 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 451..452 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 489..490 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 508..509 OTHER INFORMATION: FEATURE: NAME/KEY: Peptide LOCATION: 513..514 OTHER INFORMATION: NAME/KEY: Peptide LOCATION: 528.529 OTHER INFORMATION: Peptide 547..548 NAME/KEY: Peptide LOCATION: 431..432 OTHER INFORMATION: NAMK/KEY: Peptide LOCARION: 48..49 OTHER INFORMATION: LOCATION: 535..536 OTHER INFORMATION: NAME/KEY: Peptide FEATURE: NAME/KEY: LOCATION: RESULT 13
US-09-0%2-440-6

Sequence 6, Application US/09062440

Sequence 6, Application US/09062440

PERCENT 6.2004210:

APPLICANT: Yang, Oing

APPLICANT: Wible, Barbara A.

ITIE OF INVENTION: A Protein that Enhances Expression of

TITLE OF INVENTION: Pocassium Channels on Cell Surfaces

NUMBER OF SEQUENCES. 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calfee, Halter & Griswold LLP

STREET: Avenue

CITY: Cleveland

STATE: Ohio

SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,440 FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 2288
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEPHONE: 216228200
TELEPHONE: 216228200
INFORMATION: FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TYPE: amino acid
STRANDEDNESS: not relevant

MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: NAME/KEY: Peptide LOCATION: 37.38

ZIP: 44114
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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Sequence 10, Application US/09712495

Patent No. 6391561

GENERAL INFORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Wible, Barbara
APPLICANT: While, Barbara
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
TITLE OF INVENTION: NUMBER: US/09/712,495

TITLE OF INVENTION NUMBER: US/09/712,495

CURRENT APPLICATION NUMBER: US/09/712,495

CURRENT FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.0

SEQ ID NO 10

LENGTH: 98

LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WTCPVCDKKAPYESLIDGLFMEILXSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPGY 60
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                                                                                                                                                                                                                                                                                                                                        Query Match 93.2%; Score 506; DB 3; Length 98; Best Local Similarity 94.9%; Pred. No. 1.6e-52; Matches 93; Conservative 0; Mismatches 5; Indels
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  /note= "glycine or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (63) (63) OTHER INFORMATION: Xaa = aspartic acid or asparagine NAME/KEY: misc_feature
                                                                                                                                                                                            /note= "proline or glutamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GLDGLQYSPVQEGNQSENKKRVEVIDLTIESSSDEEDL 99
                                                                                                                                                                                                                                                                            /note= "lysine or arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (25)...(25)

OTHER INFORMATION: Xaa = serine or asparagine
NAME/KEY: misc feature
LOCATION: (61)...(61)

OTHER INFORMATION: Xaa = glycine or glutamic acid
NAME/KEY: misc_feature
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llarity 93.9%; Pred. No. 2.5e-51;
Conservative 0; Mismatches 6
                                                                                      or
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                                                                                  /note= "aspartic acid
asparagine"
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OTHER INFORMATION:
                                                                                                                                                                                                                                  Peptide
70..71
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OTHER INFORMATION:
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                                                                                                                                                                      LOCATION: 64..65
OTHER INFORMATION:
                                                              LOCATION: 63..64
OTHER INFORMATION:
OTHER INFORMATION:
                                            Peptide
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Best Local Similarity
Matches 92; Conserv
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NAME/KEY:
                                          NAME/KEY:
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                      FEATURE
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                                                                                                                                                                                                                                    Length 574;
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APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Ging
APPLICANT: Wile, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1400 McDonald Investment Center, 800 Superior STREET: 1400 McDonald Investment Center, 800 Superior STREET: Cleveland STATE: Ohio COUNTRY: US
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                                                                                                                                         ; LOCATION: 578.571
; OTHER INFORMATION: /note= "isoleucine or valine"
US-09-062-440-6
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                                                                                    /note= "alanine or serine'
OTHER INFORMATION: /note= "glycine or serine"
                                                                                                                                                                                                                                  94.1%; Score 511; DB 3;
94.9%; Pred. No. 4.3e-52;
iive O. Mismatches 5,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acida
TYPE: amino acid
TYPE: notid
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NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.9
Matches 94; Conservative
             REATURE:
NAME/KEY: Peptide
LOCATION: 548..549
OTHER LNFORMATION: /
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 25..26 OTHER INFORMATION:
                                                                                                                       NAME/KEY: Reptide LOCATION: 578,57
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LOCATION: 61..62
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US-09-062-440-10
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Pred. No. 1.9e-53;
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Patent No. 8207422

GENERAL INFORMATION:
APPLICANT: Yang, Oing
APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: A Protein Channels on Cell Surfaces
NUMBER OF SEQUENCES: A
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
                                                                                                                                      APPLICANT. Reserved.
APPLICANT. Baughn, Mariah, R.
TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
FILE REFERENCE: PC-0001 US
CURRENT APPLICATION NUMBER: US/09/836,941
CURRENT PPLICATION NUMBER: 09/286,132
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL PROGram
SEQ ID NO 2
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STREET: 1400 McDonald Investment Center, 800 Superior
STREET: Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL 461
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APPLICATION NUMBER: US/09/062,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    Sequence 2 Application US/09836941
Patent No. 6465200
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.7%;
94.9%;
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ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 4055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: -
OTHER INFORMATION: 2667068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 94.9
nes 93; Conservative
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                                                                                                                        INFORMATION:
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                                                                                                                            Sequence 4, Application US/09712495

Batent No. 6394561

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wible, Barbara
APPLICANT: Protein That Enhances Expression of Potassium Channels on Cell SU
TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell SU
TITLE OF INVENTION: And Nucleic Acids That Encode The Same
FILE REFERENCE: 22884/04046
CURRENT FILING DATE: $000-11-14
FRIOR APPLICATION NUMBER: 09/062,440
FRIOR FILING DATE: 1998/4-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
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Patent No. 6242185
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
FILE REFERENCE: PC-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.7%; Score 505; DB 4; Length 57 Best Local Similarity 94.9%; Pred. No. 1.7e-53; Matches 93; Conservative 0; Magmatches 5; Indels
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Pred. No. 1.9e-53;
0; Mismatches 5; Indels
$70 GLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL 407
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CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 17
SSCTYARE: PERL Program
SSCTYARE: PERL Program
LENGTH: 628
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Best Local Similarity 94.9
Matches 93, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-712-495-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-286-132-2
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                                                                                             RESULT 5
US-09-712-495-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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INFORMATION FOR SEQ ID NO:

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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WTCPVCDKKAPYESLIIDGLFMEILXSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPGY 60
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Sequence 6, Application US/09062440

Patent No. 6207422

GENERAL INFORMATION:

APPLICANT: Brown, Arthur M.

APPLICANT: Wible, Barbara A.

TITLE OF INVENTION: Potassium Channels on Cell Surfaces

NUMBER OF SEQUENCES: 13

CORRESPONDENCE BADBESS:

ADDRESSEE: Calfee, Halter & Griswold Lib

STREET: Avenue

CITY: Cleveland

STATE: Ohio

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOGTWARR: US

SOGTWARR: APPLICATION DATA:

TILLE OF INVERNT APPLICATION DATA:

COMPUTER: US/09/062,440

FILING DATE:

STATE: OHOO

CURRENT APPLICATION NUMBER: US/09/062,440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "glycine or glutamic acid"
                                                                                                                                                                                                                                                                                                                    NAME AND STATE OF THE STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "proline or glutamine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLDGLQYSPVQXGXPSENKKXVEVIDLTIESSSDEEDL 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LOCATION: 70..71
; OTHER INFORMATION: /note= "lymine or arginine"
US-09-062-440-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
                                                                                                                                                       not relevant
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
LOCATION: 64..65
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide LOCATION: 70..71
                                                                                                                                                                                                linear
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                                                                                                               TYPE: amino a STRANDEDNESS:
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US-09-062-440-6
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/note= "glycine or glutamic acid'
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NAME/KEY: Peptide
LOCATION: '383..384
OTHER INFORMATION: Asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 384..385
OTHER INFORMATION: Asparagine"
NAME/KEY: Peptide
LOCATION: 384..385
OTHER INFORMATION: //ote= "isoproline or glutamine"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "alanine or threonine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "alanine or threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "serine or asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "lysine or arganine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
                                                                                                                                                                                                                                                                                                                                                                                       or serine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "valine or leucine"
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                                                                                                                                                                                                                                                                                                               /note= "glycine or serine
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                                                                                                                                                                                                                                                                                                                                                                                       /note= "proline
REFERENCE/DOCKET NUMBER: 2286
TELECPHONE: 216622820
TELEPHONE: 216622820
TELEPHONE: 216622820
TELEPHONE: 216622820
TELEPHONE: 216621816
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acids
STRANDEDNESS: not relevant
TOPOLOGY: linear
TOPOLOGY: linear
MOLECLUE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: PEPTIGE
LOCATION: 37.38
LOCATION: 37.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 335.336
OTHER INFORMATION: //
FRATURE: Peptide
LOCATION: 381.382
OTHER INFORMATION:
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NAME/KEY: Peptide
LOCATION: 489.490
OTHER INFORMATION: /
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OTHER INFORMATION: /
FBATURE:
NAME/KEY: Peptide
LOCATION: 508..509
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NAME/KEY: Peptide
LOCATION: 431..432
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 41..42
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
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LOCATION: 115..116
OTHER INFORMATION:
FEATURE:
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LOCATION: 390.391
OTHER INFORMATION:
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LOCATION: 416.417
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 48..49
OTHER INFORMATION:
FEATURE:
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NAME/KEY: Peptide
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 01:30:24; Search time 14.8056 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-2 3044 1 MKIKELYRRRFPRKTLGPSD......GPLPSGPSLTGCRSDVISLD 574 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	rejues omod 5x8v80		mus	homo	homo				homo	рошо	homod	homo	Q9qyx7 mus musculu	homo		mus	_		homo	homo		rat	Q8k4j6 mus musculu	P12978 epstein-bar	homo	Q96dn6 homo sapien	rattı	Q9ulh7 homo sapien	Ξ	Q9jl04 mus musculu	Q8nez4 homo sapien	ошоч ,	homo
SUMMARIES		ID	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG HUMAN	PIAG MOUSE	NFI1 YEAST	MLL2 HUMAN		KF10_HUMAN		PCLO HUMAN		MAP4 HUMAN	HRX_MOUSE	DAG1 MOUSE	PGCN RAT	DAG1 BOVIN	MRTA HUMAN	IRS2 HUMAN	MAP4 BOVIN	ATX1_RAT	MRTA MOUSE	EBN2_EBV	Z217_HUMAN	MBD6_HUMAN	P121_RAT	MRTB_HUMAN				SAL3 HUMAN	C3G_HUMAN
		DB.	н	Н	Н	Н	Н	Н	Н	Н	Н	П	Н		Н	Н	-	Н	Н	Н	Н	н		Н			Н	Н.	Н	Н	Н	Н	Н	-	н
		Match Length	619	584	651	651	510	507	726	5262	1509	1329	1822	5147	5038	1152	3866	893	1257	895	931	1324	1072	789	964	487	1048	1003	1199	1088	1386	1567	4911	1300	1077
ok	Query	Match	9	90.3	m	m	N	N	9.6	٠		٠	•	•	4.2		٠	٠	٠					9.6			•								
		Score	2944	2749.5	1636.5	1621.5	987.5	975	263	145.5	142	133.5	129.5	128.5	127	126	125.5	125	123.5	122	121.5	121	120.5	120	119.5	611	119	118.5	118.5	118	118	118	118	117	116.5
	Result	No.	1	2	m	4	2	9	7	σ	ס יָ	010	TT.	12	13	7.4	15	16	17	18	19	20	21	22	23	4.0	57.0	9 10	7.7	7.00	62.6	0.5	31	32	33

P87253 neurospora 003172 mus musculu	Q02817 homo sapien Q03386 rattus norv	09jkq4 mus musculu PSF066 mis misculu	P20129 eggplant mo	Q62255 mus musculu Q9bxf3 homo sapien	004205 gallus gall	P13608 bos taurus O75385 homo sapien
KPC1_NEUCR ZEP1_MOUSE	MUC2_HUMAN GNDS_RAT	IRX5 MOUSE	V70K EPMV	CES2_HUMAN	TENS_CHICK	VCCA BOVIN
п п		Н Н	н,	- - -	·	4 ~
1142 2688	5179 895	484	649	1484	1744	1050
e e e e	9.8 9.8	e. e.	3.7	3.7	w .	3.7
116.5	116.5 116	115.5	113.5	113.5	113.5	113
3.4 3.5	36	38 38	0 7 6	4.4	4, 4 6, 4	45

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Best Local Similarity 91.3 Matches 524; Conservative Query Match 8 셤 ð d ò g à g ò 셤 ò This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 120 180 225 240 RNPDHSRALIKEKLTADPDSEVATTSLRVSLMCPLGKMRLTVPCRALTCAHLQSFDAALY 300 LOMNEKKPTWTCPVCDKKAPYESLIIDGLFWEILNSCSDCDEIQFMEDGSWCPMKPKKEA 360 405 SEVCPPPGYGLDGLQYSPVQEGNQSENKKRVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 420 SEVCPPPGYGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDLPPTKKHCSVTSAA 465 LOTESQHYSPSVITSLDEQDTLGHFFQFRGTPPHFLGPLAPTLGSSHRSATPAPAPGRVS 540 9 SREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE SREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE RNPDHSRALIKEKLTADPDSEVATTSLRVSLMCPLGKMRLTVPCRALTCAHLQSFDAALY 106 MHPPLPQPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQVQQILT I PAL PGSKGALTSGHQPSSVLRSPAMGTLGSDFLSSLPLHEYPPAFPLGADIQGLDLFSF 1 MKIKELYRRRPPRKTLGPSDLSLLSLPPGTSPVGSPSPLASIPPTLLTPGTLLGPKREVD MHPPLPQPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQLQQILT PKRPSRPINITPLARLSATVPNTIVVNWSSEFGRNYSLSVYLVRQLTAGTLLQKLRAKGI Gaps ·: Length 619; Indels 314 36 MIZ-TYPE. 619 AA, 67008 MW, A749A877D8925AC7 CRC64; 96.7%; Score 2944; DB 1; 96.3%; Pred. No. 1.7e-184; cive 7; Mismatches 14; SIVAPGSSLREGHGGPLPSGPSLTGCRSDVISLD 574 EMBL; AB021868; BAA78533.1; -EMBL; BC001154; AAH01154.1; -EMBL; BC030556; AAH30556.1; -EMBL; AL122061; CAB59241.1; -PIR; T34525; T34525. Pfam; PFUzozi, SAP; 1.
SNART; SMOSI3; SAP; 1.
PROCITE; PS50800; SAP; 1.
Zinc-finger; Nuclear protein. InterPro; IPR003034; SAP. InterPro; IPR004181; Znf_MIZ. Pfam; PP02037; SAP; 1. Pfam; PP02891; zf-MIZ; 1. Best Local Similarity 96.3 Matches 553, Conservative Similarity 421 46 61 121 166 181 226 241 286 301 346 361 406 481 SEQUENCE Query Match FING

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-!- SUBCELLULAR LOCATION Nuclear (By similarity).
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type zinc finger. SEQUENCE FROM N.A.

MEDIJINE=98049615; PubMed=9388184;

Chung C.D., Liao J., Liu B., Rao X., Jay P., Berta P., Shuai K

Chung C.D., Liao J., Liu B., Rao X., Jay P., Berta P., Shuai K

Scheriff Infibition of Stat3 signal transduction by PIAS3.";

Science 278:1803-1805(1997); 63652 MW; 8567831ACA1D0D98 CRC64; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
89-FEB-2003 (Rel. 41, Last annotation update)
PIAS3. or send an email to license@isb-sib.ch). MIZ-TYPE. SAP MGD; MGI:1913126; Pias3.
InterPro; IRR03034; SAP.
InterPro; IRR030181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1. Bukaryota; Metazoa; Chordata; Mammalia; Butheria; Rodentia; NCBI_TaxID=10090; EMBL; AF034080; AAB88902.2; -. Zinc-finger; Nuclear protein. DOMAIN 2 36 331 Mus musculus (Mouse) 279 3 584 AA; ZN FING SEQUENCE

240 180 SEVCPPPGYGLDGLQYSPVQEGNQSENKKRVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 420 120 190 250 300 310 360 9 77 SREVLPGAKCDYIJQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 121 SREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 1 MKIKELYRRRFPRKTLGPSDLSLLSLPPGTSPVGSPSPLASIPPTLLTPGTLLGPKREVD 46 MKIKELYRRRPPRKTLGPSDLSLPPGTSP---------61 MHPPLPQPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFTFALTPQQLQQILT -----pvhpdvtmkplpfyevygelirpttlastssqrfebahftfaltpqologilt PKRPSRPINITPLARLSATVPNTIVVNWSSEFGRNYSLSVYLVRQLTAGTLLQKLRAKGI 191 PKRPSRPINITPLARLSATVPNTIVINWSSEFGRNYSLSVYLVRQLTAGTLLQKLRAKGI RNPDHSRALIKEKLTADPDSEVATTSLRVSLMCPLGKMRLTVPCRALTCAHLQSFDAALY RNPDHSRALIKEKLTADPDSEVATTSLRVSLMCPLGKWRLTVPCRALTCAHLQSFDAALY LOMNEKKPTWTCPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEA 90.3%; Score 2749.5; DB 1; Length 584; 91.3%; Pred. No. 7.5e-172; ive 5; Mismatches 10; Indels 35; 251 78 131 181 241 301 311 g

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                                IPALPGSKGALTSGHQPSSVLRSPAMGTLGSDFLSSLPLHEYPPAFPLGADIQGLDLFSF 480
                                                             LQTESQHYSPSVITSLDEQDTLGHFFQFRGTPPHFLGPLAPTLGSSHRSATPAPAPGRVS 540
                                                                          SEVCPPPGYGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
SER-RICH.
                                                                                                                                                                                                                                                                                        Mus
                                                                                                                                                                                                                                  (DEAD/H box binding
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               ģ
                                                                                                                                                                                                                                                                                                                              DBD544128E817C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QF.
                                                                                                       574
                                                                                                                            584
                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1
PLASI OR DDXBPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X 4 AA REPEATS
                                                                                                       SIVAPGSSLREGHGGPLPSGPSLTGCRSDVISLD
                                                                                                                   SIVAPGSSLREGHGGPLPSGPSLTGCRSDVISLD
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SAP.
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InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
Repeat; Zinc-finger; Nuclear
DOMAIN
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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598
612
651 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SDEBEBERPAKRICPSLSPTSPL--SNKGILSLPHQASPVSKTPSLPAVDTSYINTSLIQ 525
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                                                 20
                                                             SLIGPKHELEL-PHITSALHPVHPDIKLOKLPFYDLLDELIKPTSLASDNSORFRETCFA
                                                                                                                                                   PALTPOOLOGILISREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCP
                                                1 MKIKELYRRRFPRKTLGPSDLSLLS-----LPPGTSPVGSPSPL----ASIPPTLLTPG
                                                                                                TIMEGPKREVDMHPPLP---QPVHPDVTMKPLPFYEVYGELIRPTTLASTSSORFEEAHFT
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                                                                                                                                                                                                     LPGYLPPTKNGAEPKRPSRPINITPLARLSATVPNTIVVNWSSEFGRNYSLSVYLVRQLT
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                        Gaps
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075925; Q99751; Q9UN02;
28-FFBB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
28-FFB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1 (Gu binding protein)
(GBP) (RNA helicase II binding protein) (DEAD/H box-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Inhibition of Statl-mediated gene activation by PIASL.";
Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liao J., Rao X., Kushner S.A., Chung C.D., Chang
          ed. No. 2.6e-99;
Mismatches 134;
            Pred. No.
57.3%; FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98393695; PubMed=9724754;
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                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651
         Best Local Similarity
Matches 349; Conserv
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SEQUENCE FROM N.A.

Length 651;

DB 1;

Score 1636.5;

53.8%;

Query Match

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HFTFALTPQQLQQILTSREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGK
                                                                                                                                                                                                                                                                                                                 563 LTGCRSDVISLD 574
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IFGIIPDIISLD 651
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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PIASG.
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                                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial, entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKIKELYRRRFPRKTLGPSDLSL-----LSLPPGTSPV----GSPSPLASIPPTLL 47
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           Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao J.,
Shuai K., French F.S.;
"Protein inhibitor of activated STAT-1 (signal transducer and
                                       activator of transcription-1) is a nuclear receptor coregulator expressed in human testis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 651;
                                                                                                        LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                           MIM; 603566; -. Gincleus; TAS. GO; GO;0005634; Cincleus; TAS. GO; GO;0003714; F:transcription co-repressor activity; TAS. GO; GO;000725; F:JAK-STAT cascade; TAS. InterPro; IPR003034; SAP. InterPro; IPR0040181; Znf. MIZ.
                               (signal transducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIZ-TYPE.
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
SER-RICH.
4 X 4 AA REPEATS OF N-T-S-L.
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4 (APPROXIMATE).
5 K (IN REF. 1).
7W - MC (IN REF. 1).
5 -> T (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1621.5; DB 1;
; Pred. No. 2.5e-98;
82; Mismatches 131;
                                                                               SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
   MEDLINE=20092325; PubMed=10628744;
                                                           Endocrinol. 14:14-26(2000).
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Pfam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
PR051T; SF05080; SAP; 1.
Repeat; Zinc-finger; Nuclear pr DOMAIN 31 383 MI DOMAIN 56 64 NU DOMAIN 368 380 NU
                                                                                                                                                                                                                                                                                                      EMBL, AF077951; AAC36702.1; -. EMBL; AF167160; AAD49722.1; -. EMBL; U78524; AAB58488.1; -. Genew; HGNC:2752; PIAS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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577
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CONFLICT
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MEDLINE=22388257; PubMed=1247932;
MEDLINE=22388257; PubMed=1247932;
MEDLINE=22388257; PubMed=1247932;
Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D. Shuai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Inhibition of Statl-mediated gene activation by PIAS1.";
Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 01:30:24; Search time 14.8056 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-4 3056 1 MKIKELYRRRFPRKTLGPSD......GPLPSGPSLTGCRSDIISLD 574 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9y6x2 homo sapien	mus m	O88907 mus musculu	075925 homo sapien	9 homo	mus r	Bacc	homo	homod	homo	mus n	рошо	homo	pos	Q9wtn3 mus musculu	epste	homo	Q9p218 homo sapien	homo	turn	homo	рошо	homo	bos t		Q04584 gallus gall	homo	homo	rattn	P08121 mus musculu	3	62910	P20129 eggplant mo
SUMMARIES	ID	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG_HUMAN	PIAG MOUSE	NFI1 YEAST	GSR1 HUMAN	MLL2 HUMAN	MBD6 HUMAN	Z297_MOUSE	MAP4 HUMAN			SRE1 MOUSE		CES2_HUMAN	KF10_HUMAN	RELB HUMAN	POLR TYMVA	MUSB_HUMAN	CAIH HUMAN	PCLO_HUMAN	PGCA_BOVIN	FMN2_MOUSE	ZYX_CHICK	C3G HUMAN	Z297 HUMAN	PGCN_RAT	CA13_MOUSE			V70K_EPMV
	DB	H	Н	Н	Н	Н	Н	-	Н	Н	Н	H	П	-4	Н	Н	Н	Ч	Н	Н	Н	Н	Н	~4		н	m	, - 4	-4	-4	H	1	1	H
	Length	619	584	651	651	510	507	726	1509	5262	1003	638	1152	1300	1072	1134	487	1484	1329	579	1844	5703	1516	5147	2364	1567	542	1077	634	1257	9	789	7	649
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	Score	3	71	1627.5	61	994.5	916	268.5	152.5	138.5	n	130	130	129	128.5	128.5	125		124.5	124	$^{\circ}$	N	122	2		2	2	N	Н	П		Н	11	117.5
	Result No.		71	m	4	Ŋ	Ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q03172 mus musculu	Q9qyx7 mus musculu	Q62255 mus musculu	P49750 homo sapien	P10358 turnip yell	P37370 saccharomyc	Q03386 rattus norv	075626 homo sapien	P10220 herpes simp	Q62165 mus musculu	P46379 homo sapien	P28477 turnip yell
ZEP1 MOUSE	PCLO MOUSE	SAL3 MOUSE	ZAP3 HUMAN	POLR TYMV	VRP1_YEAST	GNDS RAT	PRD1 HUMAN	TEGU_HSV11	DAG1 MOUSE	BAT3 HUMAN	POLR_TYMVC
г	П	7	1	1	7	7	7	Н	-	Н	7
2688	5038	1323	1822	1844	817	895	789	3164	893	1132	1844
3.8	ж. В	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.7
117.5	117	116.5	116.5	116.5	116	116	115.5	115.5	115	115	114.5
34	32	36	37	38	39	40	41	42	43	44	45

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619 AA; 67008 MW; A749A877D8925AC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 3056; DB 1; 1 Similarity 100.0%; Pred. No. 6.2e-191; 574; Conservative 0; Mismatches 0;
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EMBL; BC001154; AAH01154.1; --
EMBL; BC030556; AAH30556.1; --
EMBL; AL122061; CAB59241.1; --
PIR; T34525; T34225.
                                                                                                                                                                                                                                                                                                                                                                                                                                              | InterPro; | IPR003034; SAP. | InterPro; | IPR003034; SAP. | InterPro; | IPR004181; Znf_MIZ. | Ffam; | PP02037; SAP; 1. | Fram; | PP02891; Zf_MIZ; | SWART; SW00513; SAP; 1. | Znc_finger; | Nuclear | Procinical Property | Nuclear | Protein. | Znc_finger; | Such | Znc_finger; | Such | Znc_finger; | Such | Znc_finger; | Snch | Znc_finger; | Znc_finger;
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                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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054714;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAP.
MIZ-TYPE.
                                                                                                  Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF034080; AAB88902.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR00334; SAP.
Interpro; IPR004181; Znf_MIZ.
Pfam; PF0237; SAP; 1.
SMART; SM00513; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1913126; Pias3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50800; SAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.
                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN FING
SEQUENCE
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us-10-075-074-4.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            IPALPGSKGVLTSGHQPSSVLRSPAMGTLGGDFLSSLPLHEYPPAFPLGADIQGLDLFSF 480
                                            LQTESQHYGPSVITSLDEQDALGHFFQYRGTPSHFLGPLAPTLGSSHCSATPAPPPGRVS 540
                                                                                                                550
SEVCPPPGYGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 430
                                                                                                     LQTESQQYGPSVIISLDEQDTLGHFFQYRGTPSHFLGPLAPTLGSCHGSSTPAPPPGRVS
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WUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=B-cell;
MEDLINE=98393695; PubMed=9724454;
MEDLINE=98393695; PubMed=9724454;
Shuai K.;
Thibbition of Statl-mediated gene activation by PIASI.";
Proc. Natl. Acad. Sci. U.S.A. 95:10x26-10631(1998).
-!- FUNCTION: Specifically inhibits Activated STAT1 signaling by blocking its DNA-binding activity.
-!- SUBCELLUAR LCCATION: Nuclear (By Statlarity).
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type zinc finger.
                                                                                                                                                                                                                                                                                                                (DEAD/H box binding
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                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1
                                                                                                                                                         SIVAPGSSLREGHGGPLPSGPSLTGCRSDVISLD
                                                                                                                                           SIVAPGGALREGHGGPLPSGPSLTGCRSDIISLD
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InterPro; IPR03034; SAP.
InterPro; IPR04181; Znf MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
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Repeat; Zinc-finger; Nuclear
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PROSITE; PS50800; SAP; 1
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380
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615
523
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                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouste)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612
651 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            PIAS1 OR DDXBP1
                                                                                                                                                                                                                                            PIA1 MOUSE
                            421
                                                        431
                                                                                                             491
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ZN FING
DOMAIN
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DB 1; Length 651;

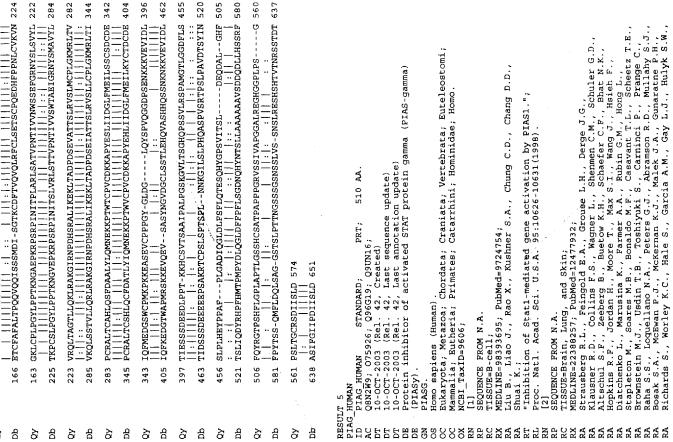
Score 1627.5;

53.3%;

Query Match

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525
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                                                                                                                                                                                                                                                                                                                     STVLLQRLRAKG\RNPDHSRALIKEKLTADSDSEIATTSLRVSLLCPLGKMRLTIPCRAL 349
                                                                                                                                                                                                                                                                                                                                                            347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SD-EEDLPPTKKHCSVTSAAIPÅLPGSKGVLTSGHQPSSVLRSPAMGTLGGDFLSSLPLH 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-QMFLDQLSAG-GSTSLPATNGSSSGSNSSLVS-SNSLRESHGHGVASRSSADTASIFG 642
                                                                                     111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565
                                                                                                                   TLLGPKREVDMHPPLP---QPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEAHFT 107
                                                          20
                                                                                                                                                                                                                                                         LPGYLPPTKNGVEPKRPSRPINITSLVRLSTTVPNTIVVSWTAEIGRTYSMAVYLVKQLS
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                                                                          MXIKELYRRRFPQKIMTPADLSIPNVHSSPMPPTLSPSTIPQLTYDGHPASSP---LLPV
                                                                                                                                                                           FALTPOQUOGILISREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVNGKLCP
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                                                       1 MKIKELYRRRFPRKTLGPSDLSLLS----LPPGTSPVGSP-----GPLAPIPPTLLAPG
                                                                                                                                  SLIGPKHELEL-PHLTSALHPVHPDIKLQKLPFYDLLDELIKPTSLASDNSQRFRETCFA
                                                                                                                                                                                                        171 FALTPOQVQQISSSMDI-SGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNTKPCS
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                          Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomh;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPSHFLGPLAPTLGSSHCSATPAPPPGRVSSLVAPGGALREGHGGPLPS
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"Inhibition of Statl-mediated gene activation by PIAS1.";
Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
                          Indels
           ed. No. 2.8e-98;
Mismatches 141;
            Pred. No.
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56.8%; P1
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                          Conservative
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         Best Local Similarity
Matches 346; Conser
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SEQUENCE FROM N.A.
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EAHFTFALTPQQVQQILTSREVLPGAKCDYTIQVQLRFCLCETSCPQEDYFPPNLFVKVN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 AA
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                                                                                                                                                                                                                                                                                                                                                                        561 PSLTGCRSDIISLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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Shuai K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SLIGPKHELEL-PHLTSALHPVHPDIKLQKLPPYDLDELIKPTSLASDNSQRFR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLAPGTLLGPKREVDMHPPLP---QPVHPDVTMKPLPFYEVYGBLIRPTTLASTSSQRFE
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                nuclear receptor coregulator
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                                                                                                                                     Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao Shuai K., French F.S.;
"Protein inhibitor of activated STAT-1 (signal transducer and
                                                                                          SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603566; -.
60; GO:0005634; C:nucleus; TAS.
GO; GO:0003714; F:transcription co-repressor activity; TAS.
GO; GO:0007259; P:JAK-STAT cascade; TAS.
InterPro; IPR003034; SAP.
InterPro; IPR004081; ZnF.
Pfam; PF02037; SAP: 1.
Pfam; PF02037; ZAP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.8%; Score 1613.5; DB 1; Length 55.7%; Pred. No. 2.3e-97; ive 78; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SER-RICH.
4 X 4 AA REPEATS OF N-T-S-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 IVV -5 MC (IN REF. 1).
13 S -5 T (IN REF. 3).
71835 MW; AA69338221124119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 (APPROXIMATE).
E -> K (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                              activator of transcription-1) is a expressed in human testis.";
   MEDLINE=20092325; PubMed=10628744;
                                                                                                               TISSUB=B-cell;
MEDLINE=97320420; PubMed=9177271;
                                                                     Endocrinol. 14:14-26(2000).
                                                                                                                                                                                                                                                                                                                                                          EMBL, AF077951; AAC36702.1; -. EMBL; AF167160; AAD49722.1; -. EMBL; U78524; AAB58488.1; -. Genew; HGNC:2752; PIAS1.
MIM; 603566; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 55.77
les 342; Conservative
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PROSITE; PS50800; SAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
380
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DOMAIN 11 4
ZN FING 331 38
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368
368
557
520
550
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651 AA;
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CONFLICT
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DOMAIN
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REPEAT
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 01:30:24; Search time 2.55357 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-5 544 1 TWTCPVCDKKAPYESLIIDG......KKKVEVIDLTIESSSDEEDL 99 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9y6x2 homo sapien	mus n	7 mus n	homo	homo	mus π	Q12216 saccharomyc	Q8uvr5 xenopus lae	_	P19070 mus musculu	Q923p0 mus musculu	P08607 mus musculu		Q9ldr9 arabidopsis				-	Q9nrl2 h bromodoma				Q04996 arabidopsis			_				80	clost	9h501 homo	Q9uig0 homo sapien
SUMMARIES	ID	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG HUMAN	PIAG MOUSE	NFI1 YEAST	BA1A XENLA	BA1B MOUSE	CR2 MOUSE	KF10 MOUSE	C4BP MOUSE	YN70 ARCFU	EX10 ARATH				EX15 ARATH	BA1A HUMAN	FERN_AZOVI	EX25_ARATH	MSTA DROME	HT31_ARATH	YF42_METKA	YOS7 CAEEL	CA11_CHICK	ITB8_RABIT	TRPD_VIBPA	HRG RABIT	BA2B HUMAN	TRPD_CLOAB	CT06_HUMAN	BA1B_HUMAN
	DB	Н	Н	Н	Н	г	Н	Н	,	~	Н	Н	Н	Н	Н							Н		, 1			H		ч	Н	٦	Н	-	٦
	Length	619	584	651	651	510	507	726	627	1479	1025	765	469	129	249	250	269	1436	248	1556	92	276	462	661	230	235	1453	768	332	526	1972	331	851	1483
οje	Query Match	0	н	60.1	σ	\sim	0	17.0	16.3	4	13.7	3	m	n	N	\sim	$^{\circ}$	$^{\circ}$	$^{\circ}$	12.5	$^{\circ}$	12.4	2	٠	12.3	12.3	12.3	12.2	12.1	12.1	12.1	11.9		11.9
	Score	544	495	327	322	257.5	222	92.5	88.5	92	74.5	73.5	72.5	72	69.5	69.5	69.5	69.5	68.5	68	67.5	67.5	67.5	67.5	67	67	67	66.5	99	99		65	65	65
	Result No.		7	m	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P39060 homo sapien	Q96pz7 homo sapien	P81901 pyrobaculum	Q92143 rhizobium m	P21817 homo sapien	Q9m2s9 arabidopsis	P56273 xenopus lae	P83332 prunus pers	P23738 mus musculu	002696 sus scrofa	Q9fjr0 arabidopsis	Q91z99 arabidopsis
CAIH HUMAN	CSM1_HUMAN	FER PYRIS	RS16 RHIME	RYR1 HUMAN	EX16 ARATH	MDM2_XENLA	TLP1 PRUPE	DCHS_MOUSE	P101 PIG	RNT1 ARATH	EXP9_ARATH
7	П	г	П	-	Н	Н	н	٦	Н	Н	1
1516	3565	101	124	5038	260	473	246	662	877	1235	258
11.9	11.9	11.9	11.9	11.9	11.7	11.7	11.6	11.6	11.6	11.6	11.5
65	65	64.5	64.5	64.5	63.5	63.5	63	63	63	63	62.5
34	35	36	37	38	39	40	41	42	43	44	4.5

N

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TWICPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=98045615; PubMed=9388184;

MEDLINE=98045615; PubMed=9388184;

"Specific 1., Liso J., Liu B., Rao X., Jay P., Berta P., Shuai K.;

"Specific 1. Into tion of Stat3 signal transduction by PIAS3.";

Science 278:1803-1805(1997).

-1- FUNCTION: Specifically inhibits activated STAT3 signaling by blocking its DNA-binding activity.

-1- SUBCELLULAR LOCATION: Nuclear (By similarity).

-1- SIMILARITY: Contains 1 SAP domain.

-1- SIMILARITY: Contains 1 MIZ-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   619 AA; 67008 MW; A749A877D8925AC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 YGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 544; DB 1;
100.0%; Pred. No. 1.3e-48;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Procein inhibitor of activated STAT protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   MIZ-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                SAP.
                                                                                                                                                                                                                                                          InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Pfam; PP02031; SAP; 1.
Pfam; PP02891; zf-MIZ.
SNART; SNG0513; SAP; 1.
PROSITE; PS50800; SAP; 1.
                                                                                                                                               EMBL, AB021868; BAA78533.1; -- EMBL, BC001154; AAH01154.1; -- EMBL, BC030556; AAH30556.1; -- EMBL; AL122061; CAB59241.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF034080; AAB88902.2; -. MGD; MGI:1913126; Pias3.
                                                                                                                                                                                                                                                                                                                                                                           Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                           PIR; T34525; T34525.
MIM; 605987; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIA3 MOUSE
054714;
                                                                                                                                                                                                                                                                                                                                                                                                                 ZN FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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PIA3_MOUSE
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                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                              319 TWICPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG 378
                                                                                                                                                                                                                                                              1 TWICPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
SAP.
MIZ-TYPE.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Euthelia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03 (Rel. 41, Created)
03 (Rel. 41, Last sequence update)
03 (Rel. 41, Last annotation update)
14 (Rel. 41, Last annotation update)
15 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
-!- FUNCTION: Specifically inhibits activated STAT1 signaling by blocking its DNA-binding activity.
-!- SUBCELLULAR LOCATION: Nuclear (Ny similarity).
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type zinc finger.
                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98393695; PubMed 9724754;
Liu B., Liao J., Rao X., Mishner S.A., Chung C.D., Chang D.D.,
Shuai K.;
                                                                                                                                                                                            Length 584;
                                                                                                                                                                          "Inhibition of Stat1-mediated gene activation by PIAS1.";
                                                                                                                            2 36 SAP.
279 331 MIZ-TYPE.
584 AA; 63652 MW; 8567831ACA1D0D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                     379 YGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDL 417
                                                                                                                                                                                                                                                                                                                                61 YGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 AA
InterPro; IPR003034; SAP.
InterPro; IPR044181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
SMART; SM0513; SAP; 1.
Zinc-finger; Nuclear Protein.
DOMAIN 2 36 SA
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        Repeat, Zinc-finger, Nuclear

        DOMAIN
        11
        45

        ZN_FING
        331
        383

        DOMAIN
        56
        64

        DOMAIN
        368
        380

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InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                                              91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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protein 1)
PIASI OR DD/BP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FRB-2003
28-FEB-2003
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                                                                                                                                            ZN FING
SEQUENCE
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          S FT KW KW
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 25, 2004, 01:30:24; Search time 14.754 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-6 2943 1 MKIKELYRRRFPRKTLGPSD......GPLPSGPSLTGCRSDIXSLD 572 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9y6x2 homo sapien			075925 homo sapien	homo	mus m	Q12216 saccharomyc	Q9nzm4 homo sapien	Q9p218 homo sapien	mus m	рошо	homod	bos t	homo	mus m	P55067 rattus norv		P12978 epstein-bar			rattus	O14686 homo sapien		P55200 mus musculu	P10220 herpes simp	Q9np71 homo sapien	oryct			neuro		Q61548 mus musculu	
SUMMARIES	αi	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG HUMAN	PIAG MOUSE	NFI1_YEAST		KF10 HUMAN	DAG1 MOUSE	MRTB HUMAN	SAL3 HUMAN	DAG1_BOVIN	DAG1 HUMAN	FMN2 MOUSE	PGCN RAT	NCO6 HUMAN	EBN2_EBV	MAP4_BOVIN	ZYX CHICK			PGCA_BOVIN	HRX_MOUSE	TEGU HSV11			CA1H HUMAN	MBD6 HUMAN	KPC1 NEUCR	ATX1 RAT		MUC2_HUMAN
	DB	н	Н	Н	Н	Н	Н	П	Н	٦	Н	-	Н	Н	Н	Н	Н	Н	Н	Н	Н		Н	H						Н			Н	Н
	Length	619	584	651	651	510	507	726	1509	1329	893	1088	1300	895	895	1567	1257	2063	487	1072	542	1574	5262	2364	3866	3164	852	895	1516	1003	1142	789	901	5179
de	Query Match	95.7	7.	0	0	30.3	0	6.9	4.8		4.1			4.0	4.0							•	3.8	٠		٠	•	٠			٠		•	3.7
	Score	2816	2573.5	1488.5	1480.5	893	881.5	204	141	130.5	120	119.5	119	118	118	117	116.5	116	115	114.5	113.5	113.5	113	112	112		110.5	110	110	109.5	109.5	108.5	108.5	108.5
	Result No.	1	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

	Q9y4h2 homo sapien Q9qyx7 mus musculu							
MUSB_HUMAN MAP4_HUMAN	IRS2_HUMAN PCLO_MOUSE	PCLO_HUMAN	Z297_HUMAN	SF01_HUMAN	TRAP_HUMAN	IRS2_MOUSE	ZAP3 HUMAN	MRTAXENLA
		٦-		7	Н	-	Н	Н
5703	1324 5038	5147	634	639	3859	1321	1822	936
3.6	3.6	9.6	3.6	3.6	3.6	3.6	3.6	3.6
108.5	107	106 5	106	106	106	105.5	105.5	105
3.4 3.5	36	38	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Ffam; PF02037; SAP; 1.
Ffam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
ZMC-finger; Nuclear protein. 95.7%; 542; Conservative Similarity ZN FING SEQUENCE 166 286 360 539 586 181 241 406 480 526 61 301 Query Match Local Matches d ð g $\overset{\circ}{\circ}$ g à qq δ d à qq ò g δ d à ò ð

584 AA.

PRT;

STANDARD;

PIA3 MOUSE ID PIA3 MOUSE

RESULT 2



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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                           Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                          SEQUENCE FROM N.A.

BEDINES-89645615; PubMed=9388184;

Chung C.D. Ligo, J., Liu B., Rao X., Jay P., Berta P., Shuai K.;

Specific inhibition of Stat3 signal transduction by PIAS3.";

"Specific inhibition of Stat3 signal transduction by PIAS3.";

"Specific 278:1803-1805(1997).

-! FUNCTION: Specifically inhibits activated STAT3 signaling by blocking its DNA-binding activity.

-! STRUCTION: Specifically inhibits in Stat3 signaling by blocking its DNA-binding activity.

-! SIMILARITY: Contains 1 SAP domain.
-! SIMILARITY: Contains 1 MIZ-type zinc finger.
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87.1%; Pred. No. 1.1e-178;
iive 6; Mismatches 31;
          , Created)
, Last sequence update)
, Last annotation update)
activated STAT protein 3
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MIZ-TYPE.
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InterPro; IPR003034; SAP.
InterPro; IPR04181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; Zf-MIZ; 1.
PROSITE; PS50800; SAP; 1.
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                                                                                             Mus musculus (Mouse),
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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DOMAIN 2 36
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Matches 500; Conservative
           28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L
28-FEB-2003 (Rel. 41, L
Protein inhibitor of ac
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Local Simi
hes 329;
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                                           479
                                                                                                                                                              550
    SEVCPPPGYGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 430
                                                                                                                                             IPALPGSKGXLTSGHQPSSVLRSPAMGTLGXDFLSSLPLHEYPPAFPLGAD1QGLDLFSF
                                                                            IPALPGSKGALTSGHQPSSVLRSPAMGTLGSDFLSSLPVHEYPPAFPLGADIQGLDLFSF
                                                                                                                        LQTES-QYXPSVITSLDEQDXLGHFFQXRFTPXHFLGPLAPTLGSSHXSATPAPXPGRVS
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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Sciurognathi, Muridae, Murinae, Mus.
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Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
-!-FUNCTION: Specifically inhibits activated STATI signaling blocking its DNA-binding activated STATI signaling blocking its DNA-binding activity.
-!- SUBCELLUIAR LOCATION: Nuclear By similarity).
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type binc finger.
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4 X 4 AA REPEATS OF N-T-S-L.
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Liu B., Liao J., Rao X., Kyshner S.A., Chung C.D.,
Shuai K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as it modified and this statement is not removed. We entities requires a license agreement (See http. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     572
                                                                                                                                                                                                                                                                                                                                                                        28-FR9-2003 (Rel. 41, Created)
28-FR9-2003 (Rel. 41, Last sequence update)
28-FR9-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1
protein 1).
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SAP.
MIZ-TYPE.
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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DOWAIN 11 45
ZN FING 331 383
DOWAIN 56 64
DOMAIN 368 380
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InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
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Pfam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
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651 AA;
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088907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMEDGSTCPMKPKKCASEVCPPPGY-GLDG-----LQYSPVQXGXPSENKKXVEVIDLTI 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSSD-EEDLPPTKKHCXVTSAAIPALPGSKGXLTSGHQPSSVLRSPAMGTLGXDFLSSL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSSSDEEEEEPPAKRICPSISPISPL--SNKGILSLPHOASPVSRIPSLPAVDISYINTS 522
                                                                        47
                                                                                                                                                                                                                                                                                                              168 CFAFALTPQQVQQISSSMDI-SGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 LIQDYRHPFHMTPMPYDLQGLDPRPFLSGDNQHYNTSLLAAAAAVSDDQDLL---HSSR
                                                                                                                                                                                                        55 MKIKELYRRRFPQKIMTPADLSIPNVH-----SSPMPPTLSPSTIPQLTYDGHPASSPL
                                                                                                                                                                              XPGTLLGPKREVDMHPPLP---OPVHPDVTMKPLPFYEVYGELIRPTTLASTSSQRFEEA
                                                                                                                                                                                                                                                                              HFTFALTPOOXQQILTSREVLPGAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGK
                                                                                                                                                                                                                                                                                                                                                                                    LCPLPGYLPPTKNGAEPKRPSRPINITPKARLSATVPNTIVVNWSSEFGRNTSLSVYLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLTAGTLLQXLRAKGIRNPDHSRALIKGKLTADPDSGVATTSLRVSLMCPLGKMRLTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLHEYPPAF---PLGADIQCLDLFSFLQTESQ-YXPSVITSL----DEQDXLGHFFQXR
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIAI HUMAN STANDARD; PRT; 651 AA. (7059751; Q9UN02; 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) 28-FBB-2003 (Rel. 41, Last annotation update) (GBP) (RNA helicase II binding protein) (GBP)/H box-binding protein (GBP)/H box-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTP----XHFLGPLAPTLGSSHXSATPAPXPGRVSSIVAPGXXLREGHGGPLPS
                        59;
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Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
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                        Indels
                                                                          1 MKIKELYRRRFPRKTLGPSDLSLLSLPPGTSPVGSPXPLAXIPPTL
.larity 53.6%; Pred. No. 3.4e-100; Conservative 74; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98393695; PubMed=9724754;
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SEQUENCE FROM N.A
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284

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LCPLPGYLPPTKNGAEPKRPSRPINITPKARLSATVPNTIVVNWSSEFGRNTSLSVYLVR 224
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             HFTFALTPQQXQQILTSREVLPGAKLDYTIQVQLRFCLCETSLPQEDYFPPNLFVKVNGK
                                                                                                                                                                                                                                                              QLTAGTLLOKLRAKGIRNPDHSRALIKGKLTADPDSGVATTSLRVSLMCPLGKMRLTVPC
                                                                                                                                                                                                                                                                                                                                                                                    RALICAHLQSFSAALYLQMNE-KPTWTCPVCDKKAPWESLIIDGLFMEILXSCSDCDEIQ
                                                168 CFAFALTPQQVQQISSSMDI-SGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNTK
                                                                                                                                                                      227 PCSLPGYLPPTKNGVEPKRPSRPINITSLVRLSTTVPNTIVVSWTAEIGRNYSMAVYLVK
                                                                                                                                                                                                                                                                                                                  287 QLSSTVLLQRLRAKGIRNPDHSRALIKEKLTADPDSBIATTSLRVSLLCPLGKMRLTIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSBEEEEPSAKRTCPSLSPTSPL--NNKGILSLPHQASPVSRTPSLPAVDTSYINTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 PLHEYPPAF----DEGADIQGLDLFSFLQTESQ-YXPSVITSL-----DEQDXLGHFFQXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 FFFYTSSQMFLDQLSAG-GSTSLPTTNGSSSGSNSSLVS-SNSLRBSHTVTNRSSTDT
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TISSUE=Brain, Lung, and Skin;

MEDLINE=22388257; Pubmed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A, Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 FMEDGSTCPMKPKKEASEVČPPPGY-GLDG-----LQYSPVQXGXPSENKKXVEVIDLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 FKEDGTWAPMRSKKEVQEV--SASYNGVDGCLSSTLEHQVASHHQSSNKNKKVEVIDLTI
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTP----XHFLGPLAPTLGSSHXSATPAPXPGRVSSIVAPGXXLREGHGGPLPS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98393695; PubMed=9724754;
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Shuai K.;
"Inhibition of S
             105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                          Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao J., Shuai K., French F.S.; "Protein inhibitor of activated STAT-1 (signal transducer and
                                                                                                                        activator of transcription-1) is a nuclear receptor coregulator expressed in human testis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                       Valdez B.C., Henning D., Perlaky L., Busch R.K., Busch H.;
"Cloning and characterization of Gu/RH-II binding protein.";
Biochem. Biophys. Res. Commun. 234:335-340(1997).
-!- FUNCTION: Specifically inhibits activated STAT1 signaling blocking its DNA-binding activity.
-!- SUBUNIT: Binds p53, RNA helicase-II and androgen receptor.
-!- SUBCELGUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Highly expressed in textis.
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 NIZ-type zinc finger.
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                                                                                                                                                                                                                       [3]
SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603566; -.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003714; F:transcription co-repressor activity; TAS.
GO; GO:0007259; P:JAK-STAT cascade; TAS.
InterPro; IPR003034; SAP.
InterPro; IPR004181; ZAI_MIZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIZ-TYPE.
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
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AA69338221124119 CRC64;
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4 (APPROXIMATE)
5 -> K (IN REF. 1).
IVV -> MC (IN REF. 1).
S -> T (IN REF. 3).
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MEDLINE=20092325; PubMed=10628744;
                                                                                                                                                                                                                                                                                                            TISSUE=B-cell;
MEDLINE=97320420; PubMed=9177271;
                                                                                                                                                                                   Endocrinol. 14:14-26(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF077951; AAC36702.1; -. EMBL; AF167160; AAD49722.1; -. EMBL; U78524; AAB58488.1; -. Genew; HGNC:2752; PIAS1. MIN; 603566; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00513; SAP; 1.
PROSTTE; PS50800; SAP; 1.
Repeat; Zinc-finger; Nuclear pi
DOMAIN 11 45 Si
ZN FING 331 383 M
DOWAIN 56 64 NU
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Matches 326; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 01:30:24; Search time 2.55357 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-7 543 1 TWTCPVCDKKAPYESLIIDG......KKRVEVIDLTIESSSDEEDL 99 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homo	mus π	O88907 mus musculu	homo	рошо	⊞us m				-		mus	_				-										Q8abi8 bacteroides		azoto	homo	291 homo	homod	omod 7zc
SUMMARIES	ID	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG_HUMAN	PIAG_MOUSE	NFI1_YEAST	BA1A_XENLA	C4BP_MOUSE	MSTA_DROME	BA1A HUMAN	BA1B_MOUSE	KF10_MOUSE	YIRF SCHPO	YN70_ARCFU	EX23_ARATH	CR2_MOUSE	EX10_ARATH	EXP1 ARATH	PHFE MOUSE	EX15_ARATH	EX25_ARATH	HT31_ARATH	PHFE_HUMAN		RYRI_HUMAN		RYR1_RABIT	FERN AZOVI	BA1B_HUMAN	RBB5_HUMAN	PR16_HUMAN	CSM1_HUMAN
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	ouery Match Length	619	584	651	651	510	507	726	627	469	462	1556	1479	765	651	129	269	1025	249	250	881	248	276	661	888	101	5038	335	5037	92	œ	538	3	26
æ	Query Match	95.2	95.0	61.1	59.7			17.5			14.1	13.8	13.6	13.4	13.3	13,1	13.0	13.0	12.8	12.8	12.8	12.6	12.6	12.6	12.3	12.1	12.1	12.0		11.9	11.9	11.8	11.8	11.8
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Q9m2s9 arabidopsis	Q86yh2 homo sapien	002696 sus scrofa	P35448 xenopus lae	Q8nez4 homo sapien	Q91z99 arabidopsis	O80932 arabidopsis	Q9pin2 campylobact	P06583 canis famil	O70400 mus musculu	Q8c156 mus musculu
EX16_ARATH	SUW2_HUMAN	P101_PIG	TSP1 XENLA	MLL3 HUMAN	EXP9 ARATH	EXP3 ARATH	ZUPT CAMJE	ATNB_CANFA	PDL1 MOUSE	CND2_MOUSE
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260	543	877	1173	4911	258	262	291	303	326	731
11.7	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.5	11.5
63.5	63	63	63	63	62.5	62.5	62.5	62.5	62.5	62.5
34	9 9 9	37	38	39	40	41	42	43	44	45

us-10-075-074-7.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 TWICPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPFG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TWICPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-98049615; PubMed-9388184;

Chung C.D., Liao J., Liu B., Rao X., Jay P., Berta P., Shuai K.;

Selence 278:1803-1805(1997).

-I- FUNCTION: Specifically inhibits activated STAT3 signaling by blocking its DNA-binding activity.

-I- SUBCELLUAR LOCATION: Nuclear (By similarity).

-I- SUBCELLUAR LOCATION: Nuclear (By similarity).

-I- SIMILARITY: Contains 1 SAP domain.

-I- SIMILARITY: Contains 1 MIZ-type zinc finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             314 366 MIZ-TYPE.
619 Aa; 67008 MW; A749AB77DB925AC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 YGLDGLQYSPVQGGDPSENKKKVEVIDLTIESSSDEEDL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGLDGLQYSPVQEGNQSENKKRVEVIDLTIESSSDEEDL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.2%; Score 517; DB 1; 94.9%; Pred. No. 3.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIA3_MOUSE STANDARD; PRT; 584 AA. 054714; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Protein inhibitor of activated STAT protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                    EMBL; AB021868; BAA78533.1; --
EMBL; BC001154; AAH01154.1; --
EMBL; BC030556; AAH30556.1; --
EMBL; AL122061; CAB59241.1; --
PIR; T34525; T34225.
                                                                                                                                                                                                                                                   MIM) 605987; -- InterPro; IPR004181; Znf_MIZ. InterPro; IPR004181; Znf_MIZ. Pfam; PF02037; SAP; 1. SMART; SM00513; Zf_MIZ; 1. SMART; SM00513; SAP; 1. PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF034080; AAB88902.2; -. MGD; MGI:1913126; Pias3.
                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger; Nuclear protein.
DOMAIN 2 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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PIA3_MOUSE
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                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                  319 TWTCPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG 378
                                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                              1 TWICPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPG
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAP.
MIZ-TYPE.
NOTCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metakoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutherik, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB 2003 (Rel. 41, Created)
28-FEB 2003 (Rel. 41, Last sequence update)
28-FEB 2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1).
PISS 10R DDXAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).

-!- FUNCTION: Specifically inhibuts activated STAT1 signaling by blocking its DNA-binding activity.

-!- SUBCELLUIAR LOCATION: Nuclear (by similarity).

-!- SIMILARITY: Contains 1 SAP domain.

-!- SIMILARITY: Contains 1 MIZ-type zigc finger.
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Liu B., Liao J., Rao X., Kachner S.A., Chung C.D., Chang D.D.,
Shuai K.;
                                                                                                                                                                                             Length 584;
                                                                                                                                                                       95.0%; Score 516; DB 1; Length 58.
96.0%; Pred. No. 4.3e-46;
Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Inhibition of Stat1-mediated gene activation by PIAS1.";
                                                                                                                        36 SAP.
331 MIZ-TYPE.
63652 MW; 8567831ACA1D0D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                    379 YGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDL 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF077950; AAC36701.1; -.
              InterPro; IPR004181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
                                                               EMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
Zinc-finger; Nuclear protein.
DOMAIN 2

        Repeat, Zinc-finger, Nuclear J

        DOWAIN
        11
        45

        ZN_FING
        331
        383
        11

        DOWAIN
        56
        64
        11

        DOMAIN
        368
        380
        11

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InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
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Pfam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                        Local Similarity 96.0
Les 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=B-cell;
MEDLINE=98393695; PubMed
InterPro; IPR003034; SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                        33
                                                                                                                                                          584 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                        ZN FING
SEQUENCE
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIA1 MOU
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
PIAL MOUSE
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   SY FEE CRAPE
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 01:30:24 ; Search time 2.52778 Seconds (without alignments) 2018.720 Million cell updates/sec Run on:

US-10-075-074-10 517 1 WTCPVCDKKAPYESLIIDGL......KKXVEVIDLTIESSSDEEDL 98 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	N O9y6x2 homo sapien	054714 mus m	E O88907 mus musculu	O75925 homo	Q8n2w9 homo	n sum 30mi6O	Q12216 sacchar	Q8uvr5 xen	P08607	E Q9z277 mus musculu			Q15291	Q91dr9	Q9c554	Q9£179	Q923p0	Q9ngc3	P54683	080622		028056	Czd960	Q9£177	Н 004996	P19070		P21817	Q8tv58	Q9h7b4	007422		31010
SUMMARIES	ID	PIA3 HUMAN	PIA3 MOUSE	PIA1 MOUSE	PIA1 HUMAN	PIAG HUMAN	PIAG MOUSE	NFIL YEAST	BA1A_XENLA	C4BP_MOUS	BA1B MOUSE	FERN_AZOVI		RBB5 HUMAN	EX10 ARATH		EX23 ARATH	KF10 MOUSE	CG1A_DROME	TAGB_DICDI	EX15 ARATH	FAH1_BACTN	ASPH_BOVIN	CSM1_HUMAN		HT31 ARATH	CR2 MOUSE		RYR1 HUMAN	YF42 METKA	SMY3 HUMAN	DRTS TOXGO	CH60 FUSIN	TINI 8 CARE
	DB	-	П	Н			Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	-	-	-		•					,		
	Length	1	584	651	651	510	507	726	627	469	1479	92	1436	538	249	250	269	765	995	1905	248	335	754	3565	276	661	1025	172	5038	230	428	610	539	591
d	ery tch		92.5	60.7	59.8	45.4	41.4	16.9	ņ.	13.5	ë	12.9	12.7	ď.	ď	ď	12.5	ď.	ς.	2	12.3	12.3	12.3	N	2	ď	12.1	'n	٠i	ij	11.7	11.7	11.6	11.6
	Score	505	478	314	309	234.5	214	87.5	81.5	70	67	66.5	65.5	65	64.5	64.5	4	64.5	64	64	63.5	63.5	63.5	ø		62.5		62	61.5	61	60.5	60.5	09	
	Result No.		7	m	4	ß	9	7	80	6	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q9fjr0 arabidopsis P15208 mus musculu	P15127 rattus norv O14129 schizosacch	O46040 drosophila P44884 haemophilus	Q28640 oryctolagus	P26013 oryctolagus	Q12094 saccharomyc	Q9hz68 pseudomonas	P09309 varicella-z
RNT1_ARATH INSR_MOUSE	INSR_RAT RA55_SCHPO	MSTA_DROME MGLA_HAEIN	HRG_RABIT	ITB8 RABIT	YOU6_YEAST	HI82_PSEAE	ICP0_VZVD
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1235 1372	1383	462 506	526	768	313	369	467
11.6	11.6	11.5	11.5	11.5	11.4	11.4	11.4
9	60 59.5	59.5	59.5	59.5	500	59	29
34 35	36	38	40	41	4 4 4 8 4 8	44	45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 WTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPGY 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GLDGLQYSPVQXGXPSENKKXVEVIDLTIESSSDEEDL 98
                                                                                                                                                                                                                                                                                                                                                                                                                 th 97.7%; Score 505; DB 1; Similarity 94.9%; Pred. No. 1.3e-48; 93; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 3.
                                                                                                                                                                                                                                                                                                                                                                   MIZ-TYPE
                                                                                                                              EMBL; AB021868; BAA78533.1; -.
EMBL; BC001154; AAH01154.1; -.
EMBL; BC030556; AAH30556.1; -.
EMBL; AL122061; CAB59241.1; -.
PIR; T34525; T34225.
                                                                                                                                                                                                                         MIM; 0.250.; InterPro; IPR003034; SAP. InterPro; IPR003034; SAP. InterPro; IPR004181; Znf_MIZ. Pfam; PP02037; SAP; 1. Pfam; PP02891; zf-MIZ; 1. SMART; SM0513; SAP; 1. PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF034080; AAB88902.2; -.
                                                                                                                                                                                                                                                                                                                                Zinc-finger; Nuclear protein. 2 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1913126; Pias3
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIA3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 054714;
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                                                                                                                                                                                                        o;
                                                                                                                                                                                                                                                         320 WTCPVCDKKAPYESLIIDGLFMEILNSCSDCDEIQFMEDGSWCPMKPKKEASEVCPPPGY 379
                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
MAZ-TYPE.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                      1 WTCPVCDKKAPYESLIIDGLFMEILXSCSDCDEIQFMEDGSWLPMKPKKEASEVCPPPGY
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1)
PIASI OR PEXEP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculda (Mouse).
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=1009q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Inhibition of Statl-mediated gene activation by PIAS1.";
Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
-!- FUNCTION: Specifically inhibits activated STAT1 signaling by blocking its DNA-binding activity.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type zinc finger.
                                                                                                                                                                                                        ,
                                                                                                                                                                        Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D. Shuai K.,
                                                                                                                                                        92.5%; Score 478; DB 1; Length 58
90.8%; Pred. No. 1.3e-45;
wiemmatches 8; Indels
                                                                                                                                         584 AA; 63652 MW; 8567831ACA1D0D98 CRC64;
                                                                                                                                                                                                                                                                                                                             380 GLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDL 417
                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                61 GLDGLQYSPVQXGXPSENKKXVEVIDLTIESSSDEEDL
                                                                                                                            MIZ-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98393695; Pubmed=9724754;
                                                                                                               SAP.
InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
SMART; SM0513; SAP; 1.
PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1913125; Pias1.
InterPro; IRR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Pfam; PP02037; SAP; 1.
SMART; SM00513; Zef_MIZ; 1.
PROSITE; PS50800; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF077950; AAC36701.1; -.
                                                                                         Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Zinc-finger; Nuclear DOMAIN 11 45
                                                                                                                                                        Juery Match
Best Local Similarity 90.00,
-hem 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                              279
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                                                                                                                                                                                                                                                                                                                                                                                                           PIA1 MOUSE
                                                                                                                           ZN FING
SEQUENCE
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DOMAIN
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